Mini Project # 6

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Contribution of each group member :

Both members worked on the questions together.

Section 1. Answers to the specific questions asked

1. Question 1

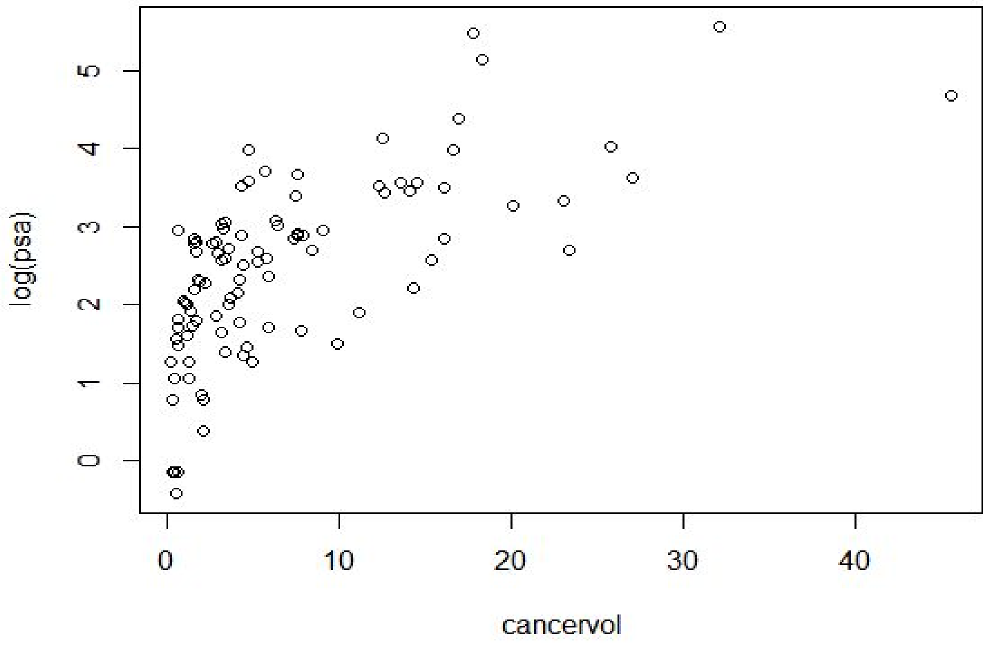
   Step 1: To build a linear model we need to analyse the linear relationship between the predictors and the response variable.

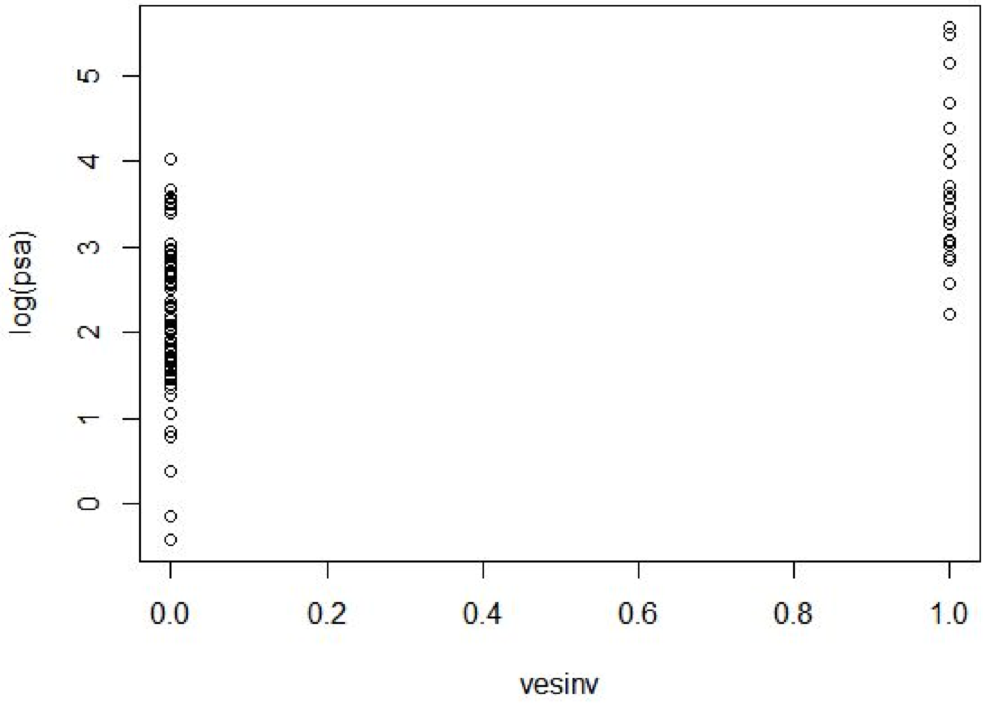
   Given: psa is the response variable and the rest of the variables are predictors.

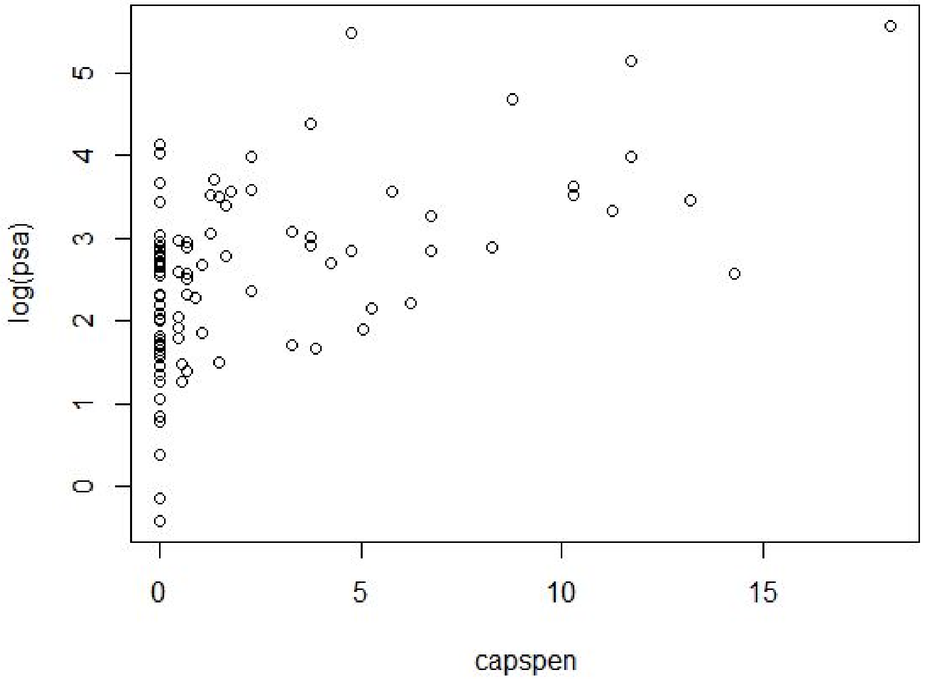
   We plot each of the predictors versus the response variable. Also, we apply log transformation for the response variable, as this transformation improves the linear relationship.

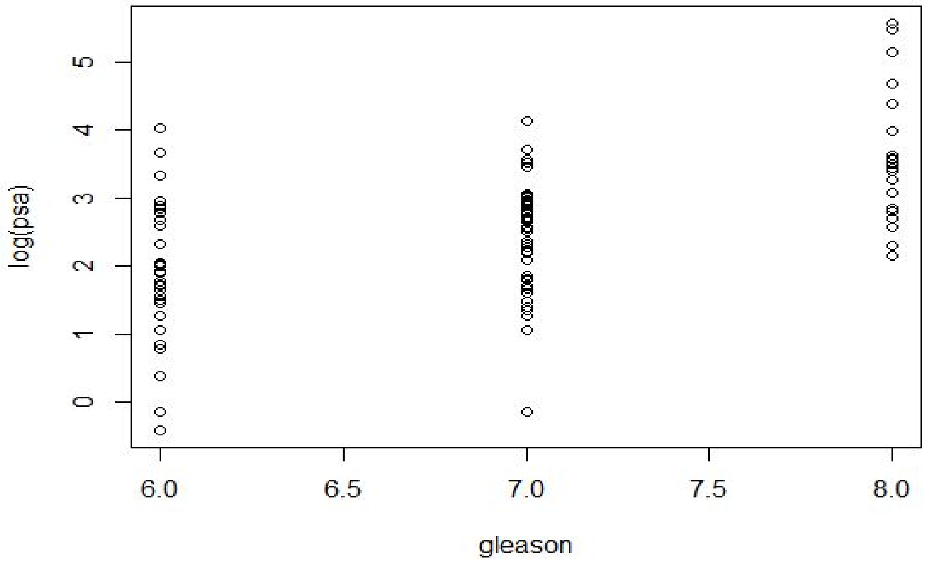
   For better understanding of the linear relationship between the variables, we have taken the correlation between the variables, which casts light upon the positive/negative linear relationship between variables. Upon, observation, there were four variables whose correlation was above 0.5 and seemed worthwhile considering.
   The variables/predictors are cancervol, vesinv, capspen, gleason.

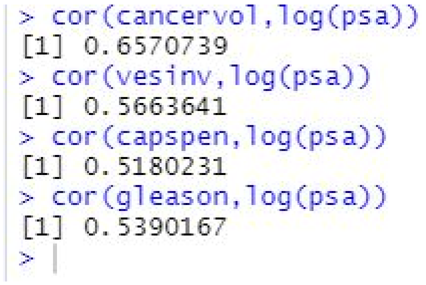
   Now we will look at their scatterplots and correlations.


log(psa)
0
1
2
3
4
5
0
10
20
30
40
cancervol


log(psa)
0
1
2
3
4
5
0.0
0.2
0.4
0.6
0.8
1.0
vesinv





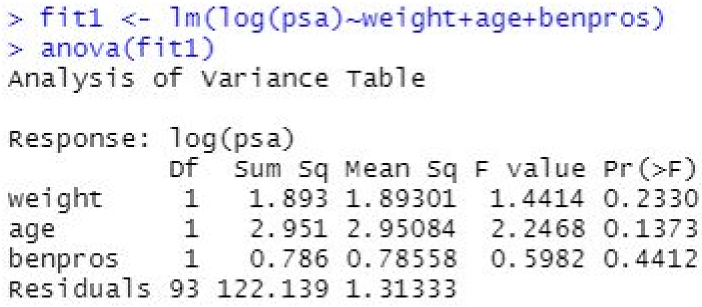


```
> cor(cancervol,log(psa))
[1] 0.6570739
> cor(vesinv,log(psa))
[1] 0.5663641
> cor(capspen,log(psa))
[1] 0.5180231
> cor(gleason,log(psa))
[1] 0.5390167
> 
```

Vesinv is a factor/qualitative variable and gleason is a quantitative variable.
As we can see, all the scatterplots show not much of a linear trend, hence we have chosen the correlation values to guide us in choosing the variables that might have an effect on the response variable.

Also, further we want to be sure about ruling out the other variables and their effects on the response variable, hence, we build a linear model to observe their p-values.
Variables we want to rule out: Weight, Age, Benpros

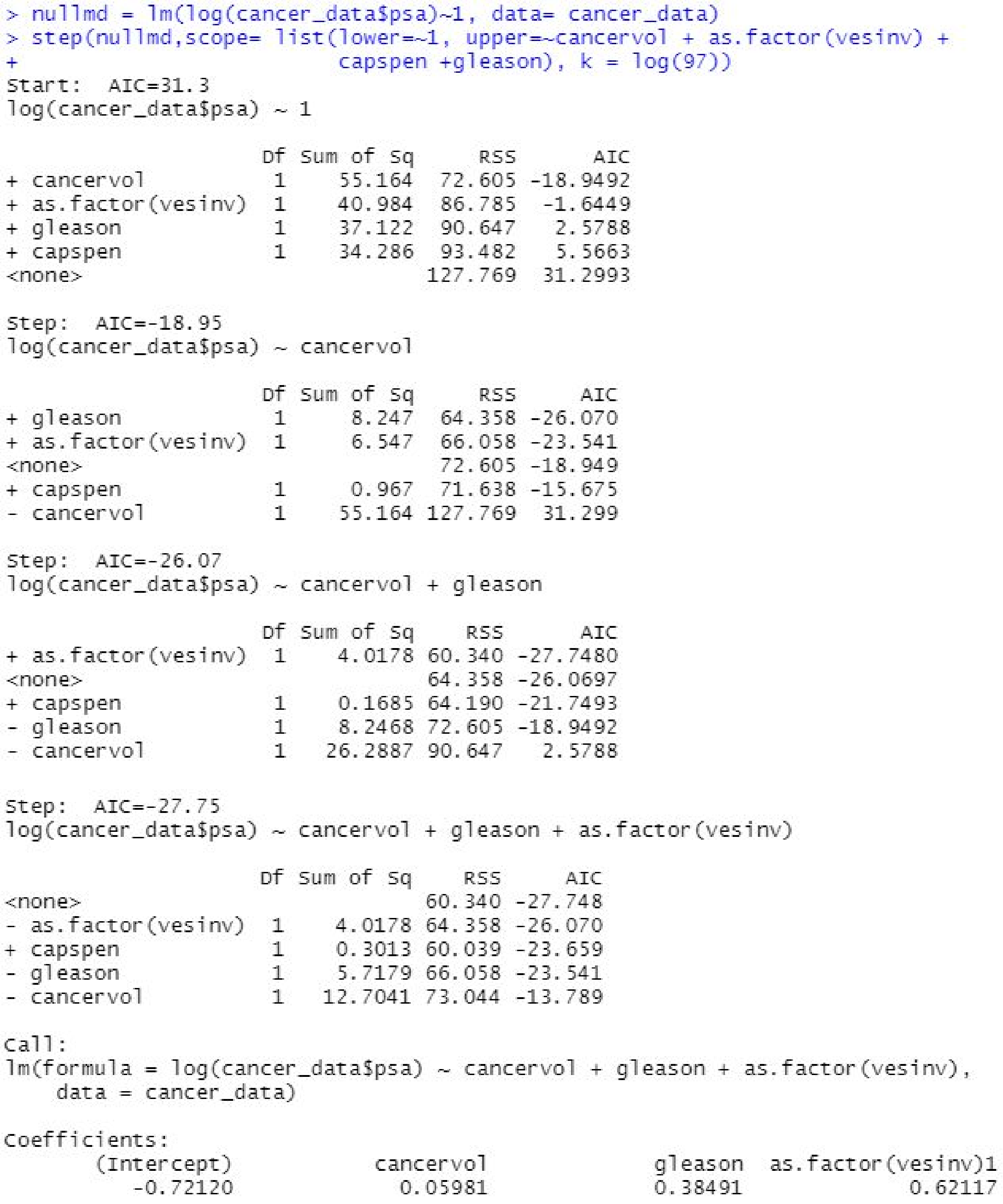
Null Hypothesis: Slope values for weight, age and benpros are zero
Alternative Hypothesis: At Least one among these variables have a slope which is non-zero



```
> fit1 <- lm(log(psa)~weight+age+benpros)
> anova(fit1)
Analysis of Variance Table

Response: log(psa)
          Df  Sum Sq Mean Sq F value Pr(>F)
weight     1   1.893 1.89301  1.4414 0.2330
age        1   2.951 2.95084  2.2468 0.1373
benpros    1   0.786 0.78558  0.5982 0.4412
Residuals 93 122.139 1.31333
```

We can clearly observe that all the three variables have a p-value >0.05 which goes on to show that we can accept the null hypothesis and reject the alternative hypothesis. When we try to build the actual model, we can avoid these three variables.

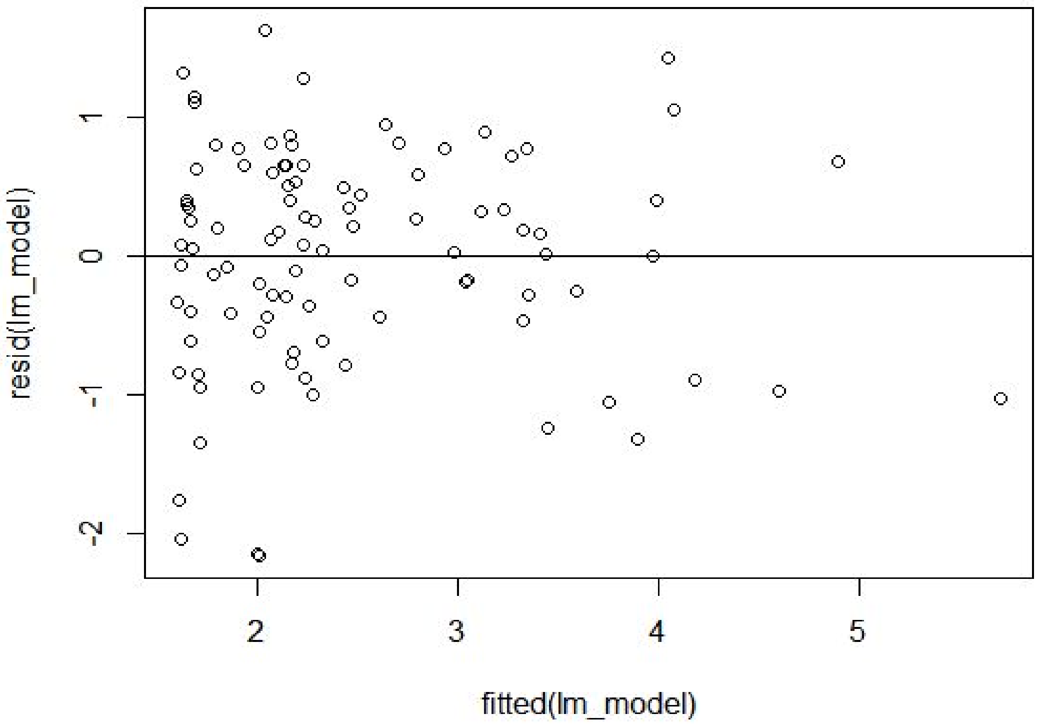
Next step is to build the linear model with the other variables available. Stepwise selection with BIC is more realistic and tries to build a decent model with minimal number of variables. Hence, we use this method.

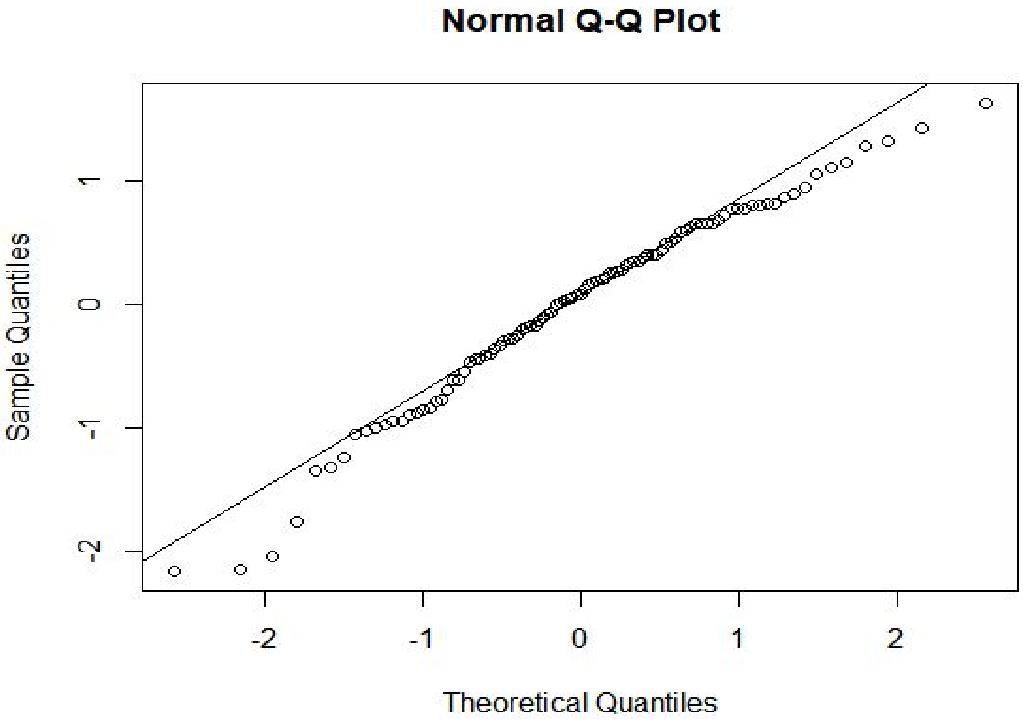


```
> nullmd = lm(log(cancer_data$psa)~1, data= cancer_data)
> step(nullmd,scope= list(lower=~1, upper=~cancervol + as.factor(vesinv) +
+                         capspen +gleason), k = log(97))
Start:  AIC=31.3
log(cancer_data$psa) ~ 1

                    Df Sum of Sq     RSS      AIC
+ cancervol          1    55.164  72.605 -18.9492
+ as.factor(vesinv)  1    40.984  86.785  -1.6449
+ gleason            1    37.122  90.647   2.5788
+ capspen            1    34.286  93.482   5.5663
<none>                           127.769  31.2993

Step:  AIC=-18.95
log(cancer_data$psa) ~ cancervol

                    Df Sum of Sq     RSS     AIC
+ gleason            1     8.247  64.358 -26.070
+ as.factor(vesinv)  1     6.547  66.058 -23.541
<none>                            72.605 -18.949
+ capspen            1     0.967  71.638 -15.675
- cancervol          1    55.164 127.769  31.299

Step:  AIC=-26.07
log(cancer_data$psa) ~ cancervol + gleason

                    Df Sum of Sq    RSS      AIC
+ as.factor(vesinv)  1    4.0178 60.340 -27.7480
<none>                           64.358 -26.0697
+ capspen            1    0.1685 64.190 -21.7493
- gleason            1    8.2468 72.605 -18.9492
- cancervol          1   26.2887 90.647   2.5788

Step:  AIC=-27.75
log(cancer_data$psa) ~ cancervol + gleason + as.factor(vesinv)

                    Df Sum of Sq    RSS     AIC
<none>                           60.340 -27.748
- as.factor(vesinv)  1    4.0178 64.358 -26.070
+ capspen            1    0.3013 60.039 -23.659
- gleason            1    5.7179 66.058 -23.541
- cancervol          1   12.7041 73.044 -13.789

Call:
lm(formula = log(cancer_data$psa) ~ cancervol + gleason + as.factor(vesinv),
    data = cancer_data)

Coefficients:
      (Intercept)           cancervol             gleason  as.factor(vesinv)1
         -0.72120             0.05981             0.38491             0.62117
```

This model has suggested us to use three predictors cancervol, gleason and vesinv(factor variable).

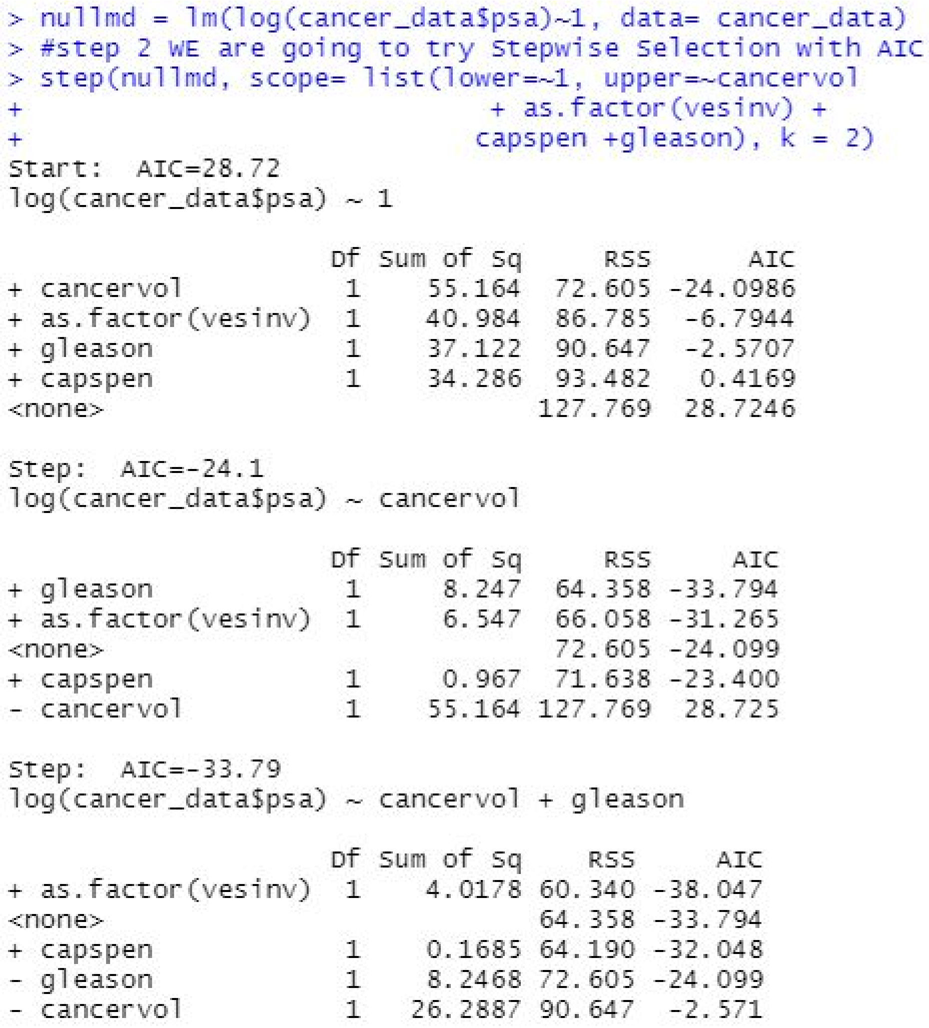
To verify if it is a good model we try to look at the fitted values and the residuals. We plot the fitted value against the residuals and also look at the QQplot for the residuals


resid(lm_model)
-2
-1
0
1
2
3
4
5
fitted(lm_model)

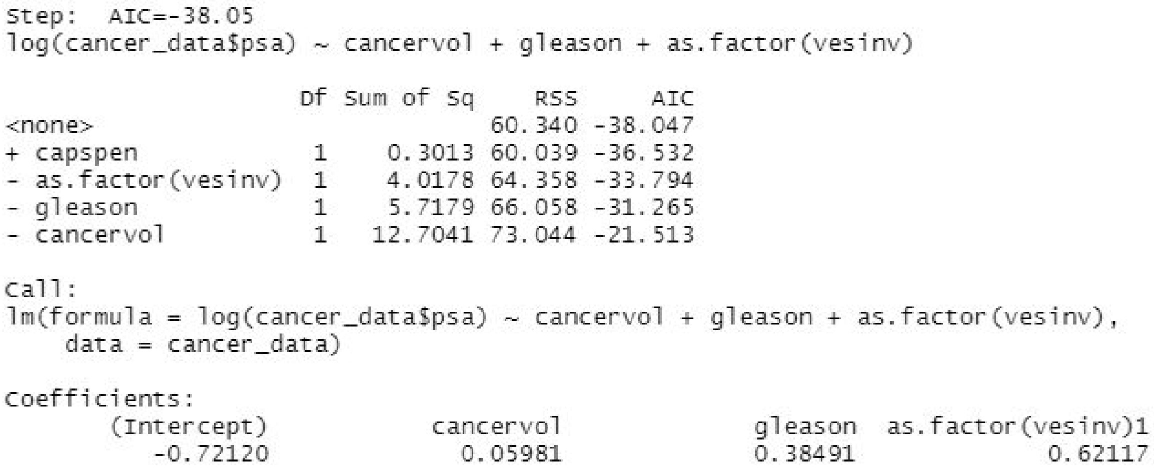

Normal Q-Q Plot
Sample Quantiles
-2
-1
0
1
-2
-1
0
1
2
Theoretical Quantiles

We observe that towards both the tails, the residuals seem to be way below the normality line.

We also want to try a stepwise model with AIC.

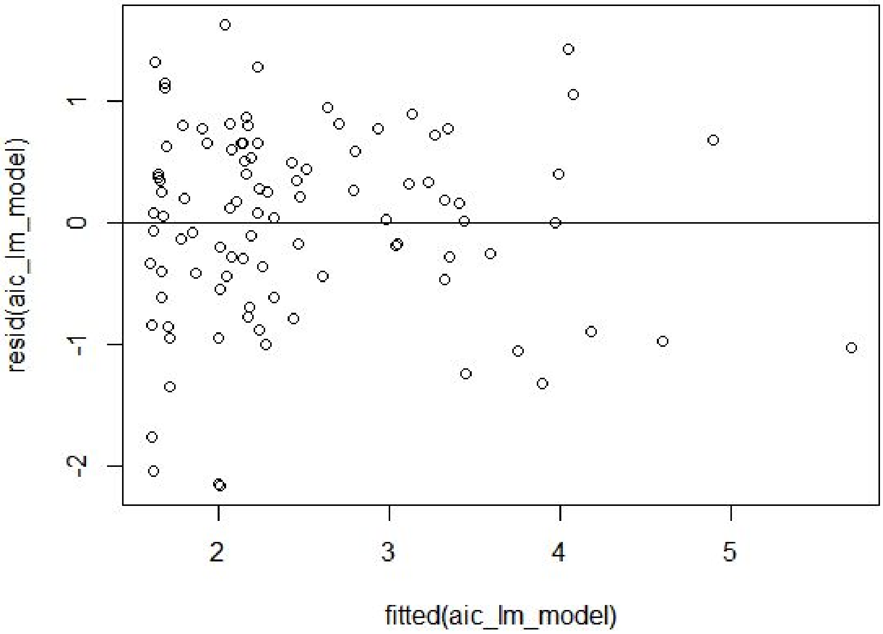


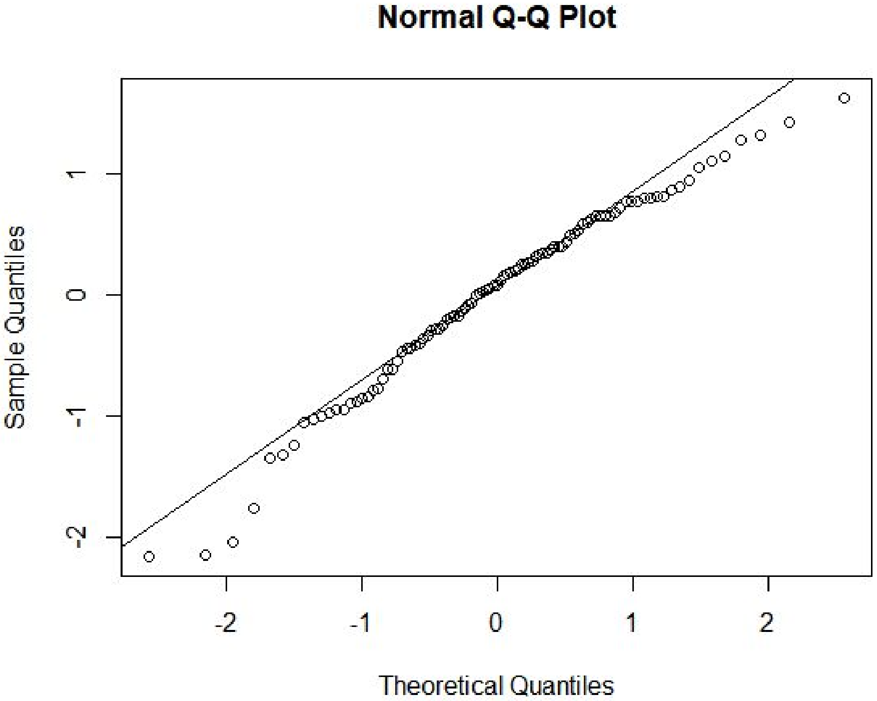
```
> nullmd = lm(log(cancer_data$psa)~1, data= cancer_data)
> #step 2 WE are going to try Stepwise Selection with AIC
> step(nullmd, scope= list(lower=~1, upper=~cancervol
+                              + as.factor(vesinv) +
+                             capspen +gleason), k = 2)
Start:  AIC=28.72
log(cancer_data$psa) ~ 1

                    Df Sum of Sq     RSS      AIC
+ cancervol          1    55.164  72.605 -24.0986
+ as.factor(vesinv)  1    40.984  86.785  -6.7944
+ gleason            1    37.122  90.647  -2.5707
+ capspen            1    34.286  93.482   0.4169
<none>                           127.769  28.7246

Step:  AIC=-24.1
log(cancer_data$psa) ~ cancervol

                    Df Sum of Sq     RSS     AIC
+ gleason            1     8.247  64.358 -33.794
+ as.factor(vesinv)  1     6.547  66.058 -31.265
<none>                            72.605 -24.099
+ capspen            1     0.967  71.638 -23.400
- cancervol          1    55.164 127.769  28.725

Step:  AIC=-33.79
log(cancer_data$psa) ~ cancervol + gleason

                    Df Sum of Sq    RSS     AIC
+ as.factor(vesinv)  1    4.0178 60.340 -38.047
<none>                           64.358 -33.794
+ capspen            1    0.1685 64.190 -32.048
- gleason            1    8.2468 72.605 -24.099
- cancervol          1   26.2887 90.647  -2.571
```



```
Step:  AIC=-38.05
log(cancer_data$psa) ~ cancervol + gleason + as.factor(vesinv)

                    Df Sum of Sq    RSS     AIC
<none>                           60.340 -38.047
+ capspen            1    0.3013 60.039 -36.532
- as.factor(vesinv)  1    4.0178 64.358 -33.794
- gleason            1    5.7179 66.058 -31.265
- cancervol          1   12.7041 73.044 -21.513

Call:
lm(formula = log(cancer_data$psa) ~ cancervol + gleason + as.factor(vesinv), 
    data = cancer_data)

Coefficients:
      (Intercept)          cancervol            gleason  as.factor(vesinv)1  
         -0.72120            0.05981            0.38491             0.62117  
```

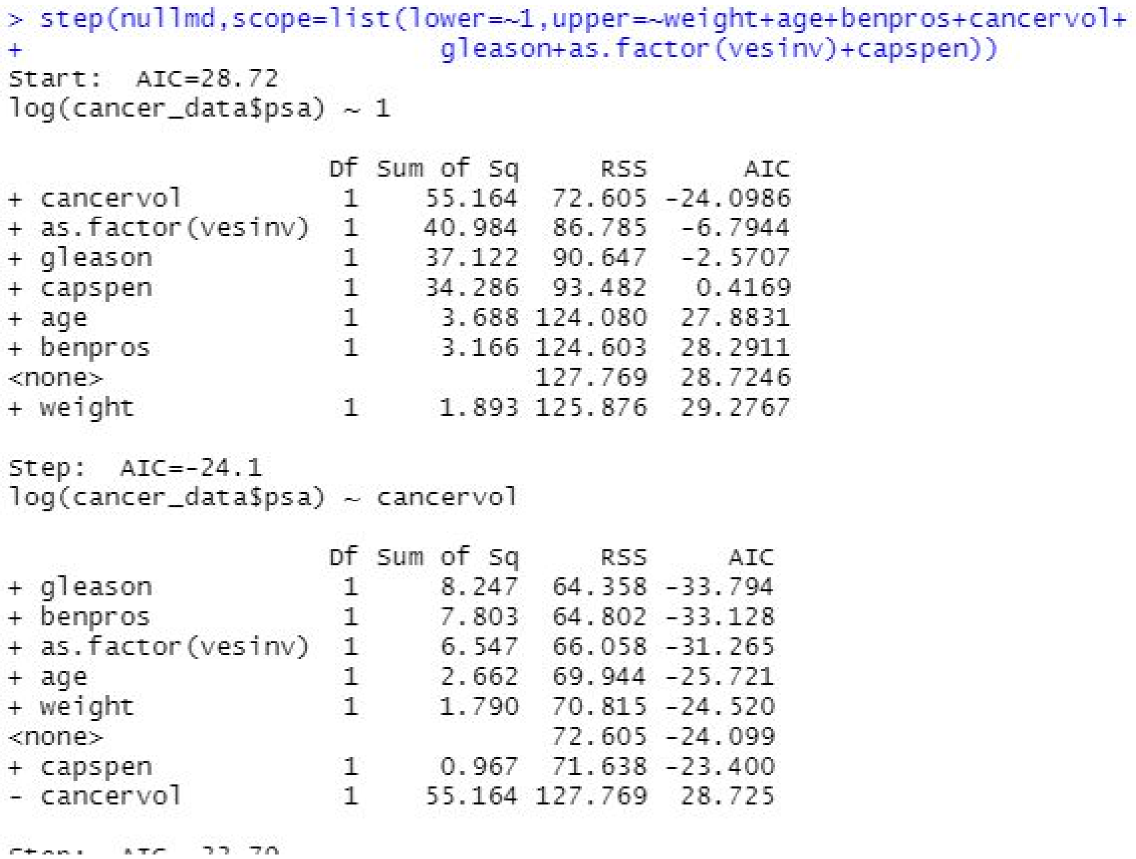
Below are the residual vs fitted scatterplot, and qqplot for the residuals.



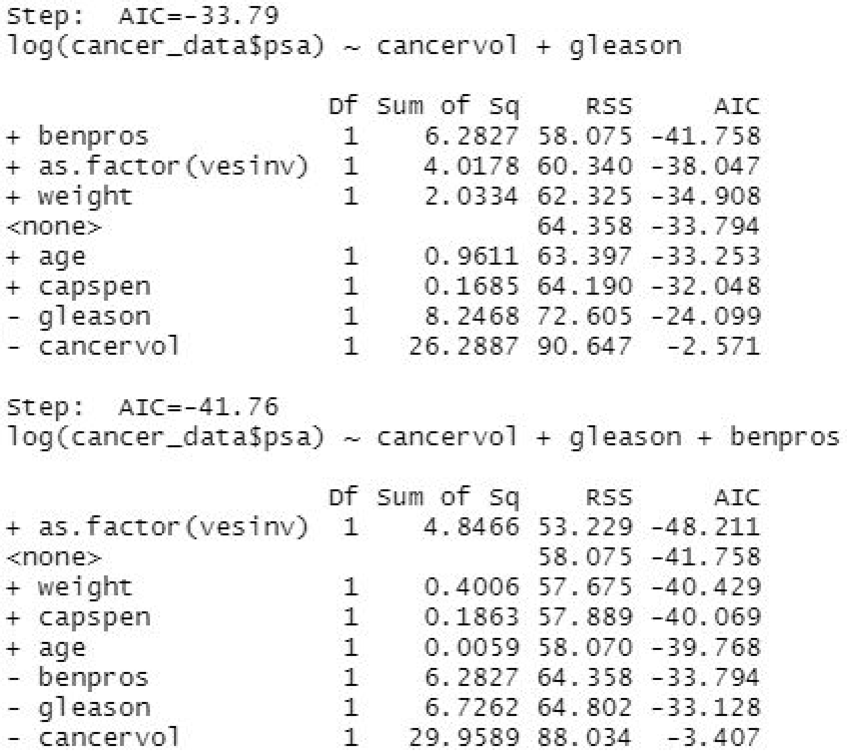


These plots are very similar to the Stepwise selection model calculated with BIC.

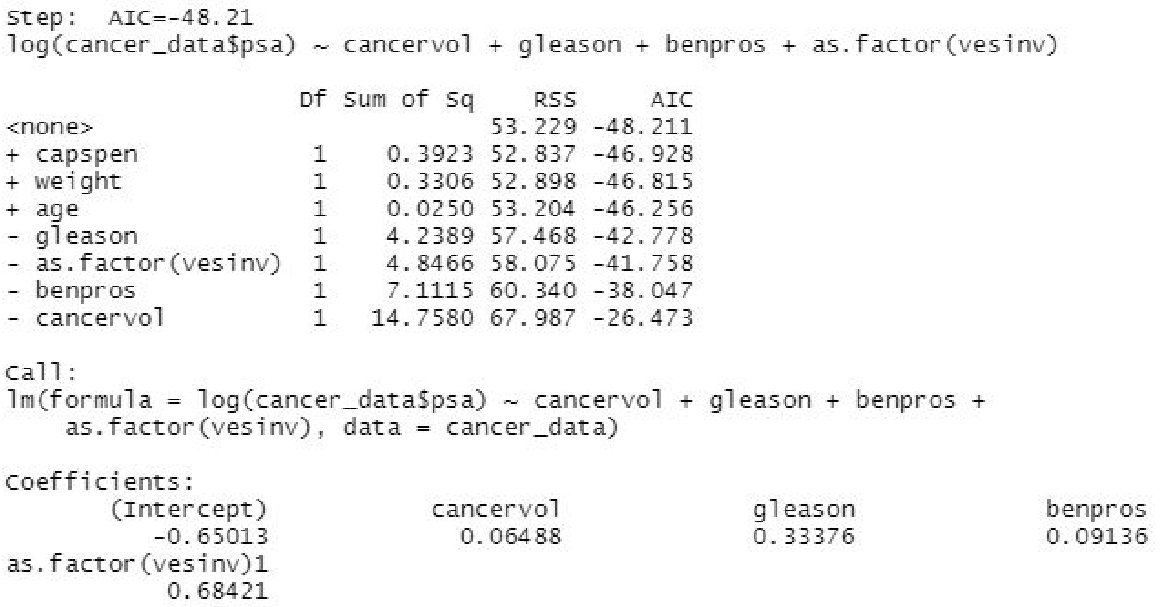
Though we initially ruled out three variables, we would like to build a stepwise selection with all variables to see if there is any significant improvement in the model result.



```
> step(nullmd,scope=list(lower=~1,upper=~weight+age+benpros+cancervol+
+                          gleason+as.factor(vesinv)+capspen))
Start:  AIC=28.72
log(cancer_data$psa) ~ 1

                    Df Sum of Sq     RSS      AIC
+ cancervol          1    55.164  72.605 -24.0986
+ as.factor(vesinv)  1    40.984  86.785  -6.7944
+ gleason            1    37.122  90.647  -2.5707
+ capspen            1    34.286  93.482   0.4169
+ age                1     3.688 124.080  27.8831
+ benpros            1     3.166 124.603  28.2911
<none>                           127.769  28.7246
+ weight             1     1.893 125.876  29.2767

Step:  AIC=-24.1
log(cancer_data$psa) ~ cancervol

                    Df Sum of Sq     RSS     AIC
+ gleason            1     8.247  64.358 -33.794
+ benpros            1     7.803  64.802 -33.128
+ as.factor(vesinv)  1     6.547  66.058 -31.265
+ age                1     2.662  69.944 -25.721
+ weight             1     1.790  70.815 -24.520
<none>                            72.605 -24.099
+ capspen            1     0.967  71.638 -23.400
- cancervol          1    55.164 127.769  28.725
```

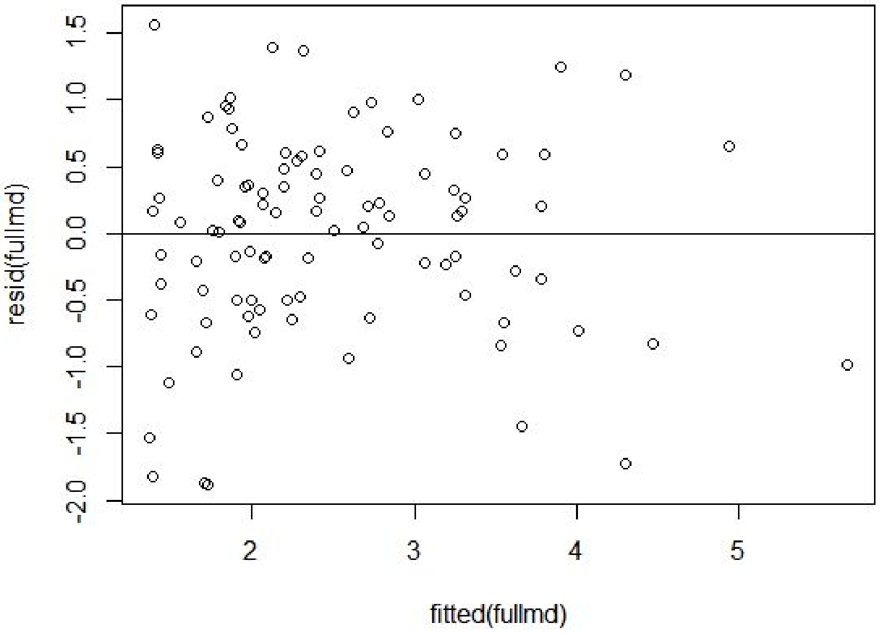


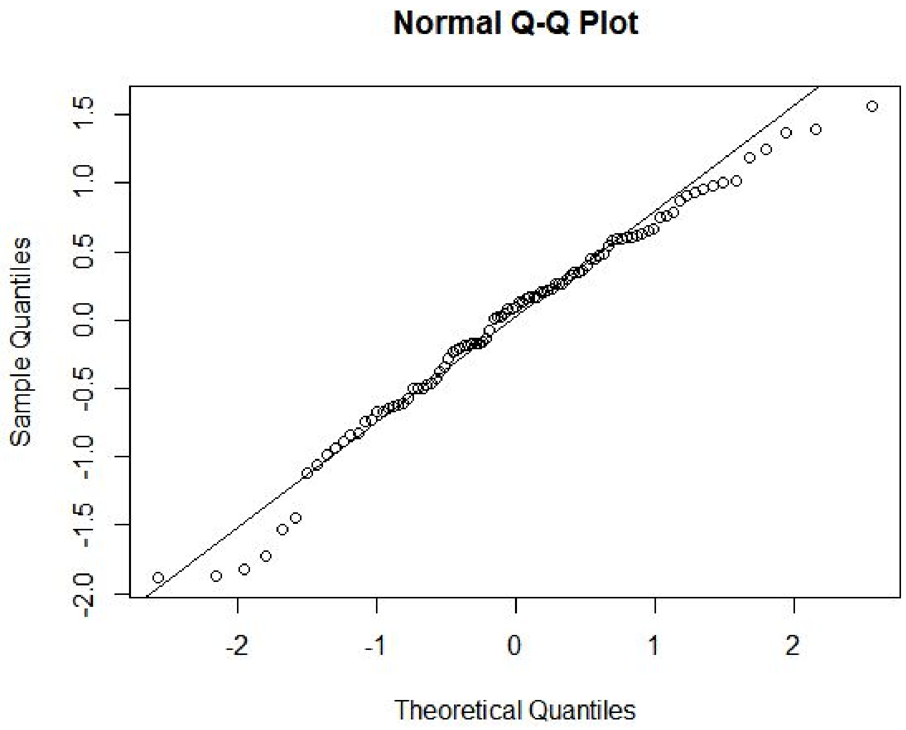
```
Step:  AIC=-33.79
log(cancer_data$psa) ~ cancervol + gleason

                    Df Sum of Sq    RSS     AIC
+ benpros            1    6.2827 58.075 -41.758
+ as.factor(vesinv)  1    4.0178 60.340 -38.047
+ weight             1    2.0334 62.325 -34.908
<none>                           64.358 -33.794
+ age                1    0.9611 63.397 -33.253
+ capspen            1    0.1685 64.190 -32.048
- gleason            1    8.2468 72.605 -24.099
- cancervol          1   26.2887 90.647  -2.571

Step:  AIC=-41.76
log(cancer_data$psa) ~ cancervol + gleason + benpros

                    Df Sum of Sq    RSS     AIC
+ as.factor(vesinv)  1    4.8466 53.229 -48.211
<none>                           58.075 -41.758
+ weight             1    0.4006 57.675 -40.429
+ capspen            1    0.1863 57.889 -40.069
+ age                1    0.0059 58.070 -39.768
- benpros            1    6.2827 64.358 -33.794
- gleason            1    6.7262 64.802 -33.128
- cancervol          1   29.9589 88.034  -3.407
```



```
Step:  AIC=-48.21
log(cancer_data$psa) ~ cancervol + gleason + benpros + as.factor(vesinv)

                    Df Sum of Sq    RSS     AIC
<none>                           53.229 -48.211
+ capspen            1    0.3923 52.837 -46.928
+ weight             1    0.3306 52.898 -46.815
+ age                1    0.0250 53.204 -46.256
- gleason            1    4.2389 57.468 -42.778
- as.factor(vesinv)  1    4.8466 58.075 -41.758
- benpros            1    7.1115 60.340 -38.047
- cancervol          1   14.7580 67.987 -26.473

Call:
lm(formula = log(cancer_data$psa) ~ cancervol + gleason + benpros + 
    as.factor(vesinv), data = cancer_data)

Coefficients:
       (Intercept)           cancervol             gleason             benpros  
          -0.65013             0.06488             0.33376             0.09136  
as.factor(vesinv)1  
           0.68421  
```

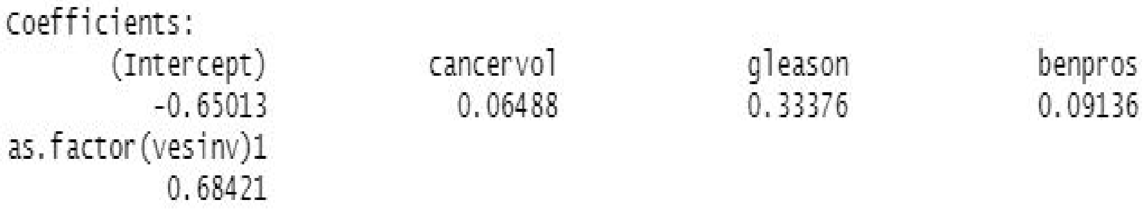
We can observe that the three variables we initially rejected are not included in the model, but all the other variables are available. To see if this is a better model, we look at the fitted vs residual scatter plots and the qq plot for residuals.





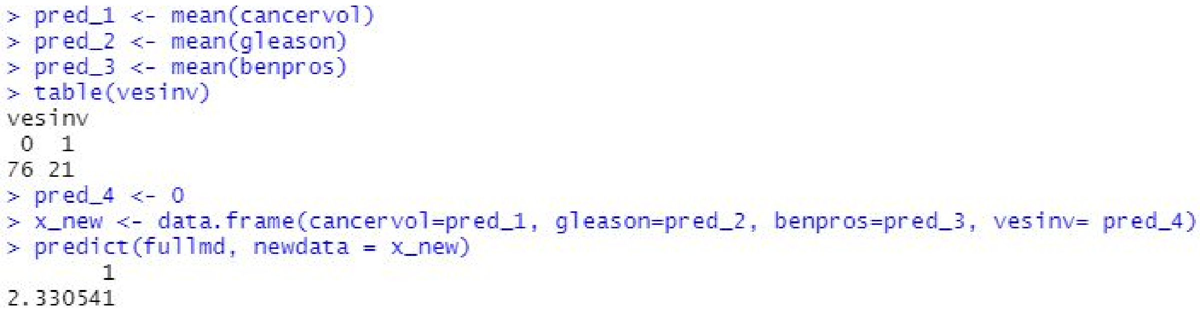
We can clearly see from the qqplot, the residuals show a significantly better normal plot and hence, the final model is inclusive of these four predictors(cancervol,gleason,benpros,vesinv)

The regression result is:



```
Coefficients:
      (Intercept)          cancervol          gleason          benpros
         -0.65013            0.06488          0.33376          0.09136
as.factor(vesinv)1
          0.68421
```

The predicted value for psa according to specifications given is



```
> pred_1 <- mean(cancervol)
> pred_2 <- mean(gleason)
> pred_3 <- mean(benpros)
> table(vesinv)
vesinv
 0  1
76 21
> pred_4 <- 0
> x_new <- data.frame(cancervol=pred_1, gleason=pred_2, benpros=pred_3, vesinv= pred_4)
> predict(fullmd, newdata = x_new)
       1
2.330541
```

Equation =
-0.65013+(0.06488*pred_1)+(0.33376*pred_2)+(0.09136*pred_3)+(0.68421*pred_4)

Predicted_Psa = 2.330541

Section 2: R code.

R code for question 1

```
#mini project 6
#Team members
#Qingyu Lan
#Lakshmi Priyanka Selvaraj

#Q1
rm(list =ls())
setwd("D:/UTD/Fall_2020/1. Statistical Methods of Data Science/Project work")

cancer_data <- read.csv("prostate_cancer.csv")
head(cancer_data)
str(cancer_data)

#First and foremost is we try to plot and observe linear trends
attach(cancer_data)
plot(cancervol,log(psa))
cor(cancervol,log(psa))
plot(weight,log(psa))
cor(weight,log(psa))
plot(age,log(psa))
cor(age,log(psa))
plot(benpros,log(psa))
cor(benpros,log(psa))
plot(vesinv,log(psa))
cor(vesinv,log(psa))
plot(capspen,log(psa))
cor(capspen,log(psa))
plot(gleason,log(psa))
cor(gleason,log(psa))

#None of the above variables show a linear trend with the psa-response variable

cor(cancervol,psa)
```

```
#The variables Cancervol and psa seem to have a strong positive correlation though


table(cancer_data$vesinv)
table(cancer_data$gleason)

#We are going to try some individual variables
fit1 <- lm(log(psa)~weight+age+benpros)

summary(fit1)

anova(fit1)

step(nullmd,scope=list(lower=~1,upper=~weight+age+benpros))


#Step 1 I am going to try Stepwise Selection with BIC

nullmd = lm(log(cancer_data$psa)~1, data= cancer_data)
nullmd

step(nullmd,scope= list(lower=~1, upper=~cancervol + as.factor(vesinv) +
               capspen +gleason), k = log(97))

lm_model <- lm(formula = log(cancer_data$psa) ~ cancervol + gleason + as.factor(vesinv),
         data = cancer_data)

fitted(lm_model)
resid(lm_model)

plot(fitted(lm_model),resid(lm_model))
abline(h=0)

qqnorm(resid(lm_model))
qqline(resid(lm_model))


#step 2 WE are going to try Stepwise Selection with AIC
step(nullmd, scope= list(lower=~1, upper=~cancervol
                 + as.factor(vesinv) +
                capspen +gleason), k = 2)


aic_lm_model <- lm(formula = log(cancer_data$psa) ~ cancervol + gleason +
as.factor(vesinv),
            data = cancer_data)
```

```
plot(fitted(aic_lm_model),resid(aic_lm_model))
abline(h=0)

qqnorm(resid(aic_lm_model))
qqline(resid(aic_lm_model))

#Stepwise selection with BIC
nullmd = lm(log(cancer_data$psa)~1, data= cancer_data)
step(nullmd,scope=list(lower=~1,upper=~weight+age+benpros+cancervol+
                    gleason+as.factor(vesinv)+capspen))

fullmd <- lm(formula = log(cancer_data$psa) ~ cancervol + gleason + benpros +
            as.factor(vesinv), data = cancer_data)

plot(fitted(fullmd),resid(fullmd))
abline(h=0)

qqnorm(resid(fullmd))
qqline(resid(fullmd))


#Prediction 3 quantitative variables, 1 qualitative variable
pred_1 <- mean(cancervol)
pred_2 <- mean(gleason)
pred_3 <- mean(benpros)
table(vesinv)

pred_4 <- 0

x_new <- data.frame(cancervol=pred_1, gleason=pred_2, benpros=pred_3, vesinv= pred_4)

predict(fullmd, newdata = x_new)
```